INTRODUCTION

The name Mollusc (=Mollusk) was derived from Latin mollus meaning soft. The first mollusc appeared as far back as the Cambrian period, approximately 500 million years ago. 3370 species of molluscs were recorded from marine environment (**Venkataraman and Wafer, 2005**).

Molluscs fishery comprise mainly by bivalves such as clams, mussels and oysters. They have been exploited worldwide for food, ornamentation, medicinal uses and pearls throughout human history (**CSIR, 1962**). The abundance and diversity of bivalves have made them attractive subject for both zoologists and paleontologists. Despite the long scientific interest in bivalves, the relationships between its members are perhaps surprisingly unresolved and even more recent schemes are often deeply conflicting **(Morton, 1996 and Amler, 1999).**

The largest and recent family of Bivalvia, the marine Veneridae with approximately 800 species, comprises one of the least understood and most poorly defined molluscan taxa, despite including some of the most economically important and abundant bivalves **(Mikkel, *et al.*, 2006)**.

The classification within the family has been controversial at least since the 1930s. The most used classification is that of **Keen (1969)** which recognized 12 subfamilies. Some common species have been moved between genera because of repeated attempts to bring a more valid organization to the classification or taxonomy of the family; therefore changes in the generic name of species are frequently encountered.

The characters used for classifying this group still tend to be superficial, focusing on external features, especially those of the shell, which are adapted to their environment. Recently the morphological characters are evaluated by mapping them onto the resultant phylogenetic tree by **Kappner and Bieler (2006)**. Morphological analyses using 45 exemplar taxa and 23 traditional characters are highly failed to reconstruct traditional veneroid classification **(Mikkel, *et al*., 2006).** All the previous works encourage and through the light on the molecular genetic characters as a valuable insights for phylogenetic studies. Nucleotide sequences characteristically provide high numbers, usually hundreds or even thousands of characters of little but equal complexity. They form data sets independent from morphological data, as postulated by **Harper, *et al.* (2000)**, because DNA sequences are less selected by lifestyle and habitat than morphology.

Venerids are considered one of the favourite seafoods especially for the people who mainly inhabit the cities located on marine coasts. They have high value of protein and fair amount of calcium and iron (**El-Gamal, 1988**). These clams, which are commonly eaten, may be either harvested from the wild or produced in aquaculture. They tend to thrive in shelter marine environments, frequently near shore, where nutrient levels are high; thus there is a strong possibility that the live animals may be contaminated with sewage derived pathogens as well as those from the general environment (heavy metals, hydrocarbons and pesticides) **(El-Shenawy, 2004 and El-Shenawy *et al.*, 2009)**.

Moreover, the fact that venerids are filter feeders and good indicators for monitoring the pollution in the surrounding environment. They extract the contaminants with the extracting oxygen and food and accumulate them in their bodies much higher than in the surrounding sea water (**Farag *et al.*, 2000; El-Gamal & Sharshar, 2004 and Hamed& Emara, 2006**).

So attention has been recently drawn to not only the phylogenetic map but also to the goals of genetic ecotoxicology, in particular, the need to relate genotoxicity in individuals to population and community level. The concept that genetic patterns within populations may be altered by exposure to contaminants is not novel **(Klerks & Weis, 1987; De Wolf *et al.*, 2004 and Liyan *et al.*, 2005).** All of these works emphasized that links between conservation genetics and genetic ecotoxicology provide powerful tools to address the environmental effect of contaminants.

Due to the above circumstances identification and phyletic relationships between the members within Veneridae is urgent to construct database. This study aims to construct genetic maps to follow any genetic variations.

AIM OF THE WORK:

The present study aims to:

1. Identify venerids from different habitats of the Egyptian marine water by using morphological and genetical characters to construct an identification key for their separation and to declare their taxonomic relationship.
2. Determine some ecological factors including physico-chemical parameters, heavy metals and total petroleum hydrocarbons in the different stations where the venerids inhabit.
3. Examine the cause of noticeable accumulation of venerid dead shells over some marine coasts, by using the histopathological study.
4. Assess the genetic diversity of one popular venerid species collected from polluted and unpolluted areas, to formulate hypotheses regarding the underlying mechanism that is responsible for its population genetic structure.